



- 1 -

SEQUENCE LISTING

<110> Willson, Tracey
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Hilton, Douglas
Metcalf, Donald
Zhang , Jian

<120> A novel haemopoietin receptor and genetic sequences encoding same

<130> 23199-215

<140> US 09/688,286

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<150> AU PN6135
<151> 1995-10-23

<150> AU PN7276
<151> 1995-12-22

<150> AU PP2208
<151> 1996-09-09

<160> 12

<170> PatentIn version 3.1

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<212> DNA
<213> Mus musculus

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<222> (61) .. (1332)
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Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Trp
1 5 10 15

acc gcc acc gtg ggc caa gtt gcc gcg gcc aca gaa gtt cag cca cct 156
Thr Ala Thr Val Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro Pro
20 25 30

gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata tgg 204
Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp
35 40 45

acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga tat 252
Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr
50 55 60

ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa act Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr 65 70 75 80	300
cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag gtg His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val 85 90 95	348
ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg gtg Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val 100 105 110	396
aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg act Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr 115 120 125	444
gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc tgg Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp 130 135 140	492
ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac tat Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr 145 150 155 160	540
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gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa cct Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro 180 185 190	636
agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat gct ggg Ser Phe His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly 195 200 205	684
aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat gtg aaa Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys 210 215 220	732
cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt gcc tta Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu 225 230 235 240	780
tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc tta act Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr 245 250 255	828
tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat att tta Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu 260 265 270	876
gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga aac atg Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met 275 280 285	924
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Tyr	Thr	Val	Arg	Val	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Phe	Asp	Asp		
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35 40 45

Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr
50 55 60

Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr
65 70 75 80

His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val
85 90 95

Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val
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Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr
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Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp
130 135 140

Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr
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Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg
165 170 175

Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro
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Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly
195 200 205

Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys
210 215 220

Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu
225 230 235 240

Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr
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260 265 270

Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met
275 280 285

Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val
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Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp
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Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu
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Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe
340 345 350

Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys
355 360 365

Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu
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Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp
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 Ala Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
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 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
 Pro Val Thr Asn Leu Ser Val Val Glu Asn Leu Cys Thr Val Ile
 35 40 45
 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
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 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
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 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
 100 105 110
 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125
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 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
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 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
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 Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
 165 170 175
 aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag 636
 Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
 180 185 190
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 Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
 195 200 205

gca gga aaa att aaa cca tcc ttc aat ata gtg cct tta act tcc cgt Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg 210 215 220	732
gtg aaa cct gat cct cca cat att aaa aac ctc tcc ttc cac aat gat Val Lys Pro Asp Pro His Ile Lys Asn Leu Ser Phe His Asn Asp 225 230 235 240	780
gac cta tat gtg caa tgg gag aat cca cag aat ttt att agc aga tgc Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys 245 250 255	828
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gtt ttc tac gtc caa gag gct aaa tgt gag aat cca gaa ttt gag aga Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg 275 280 285	924
aat gtg gag aat aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp 290 295 300	972
act ttg aac aca gtc aga ata aga gtc aaa aca aat aag tta tgc tat Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr 305 310 315 320	1020
gag gat gac aaa ctc tgg agt aat tgg agc caa gaa atg agt ata ggt Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly 325 330 335	1068
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ctg ata gaa aac ctg aag aaa gcc tct cag tgatggagat aattttatTTT Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln 420 425	1358
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35 40 45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
50 55 60

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
65 70 75 80

Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
85 90 95

Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
100 105 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
115 120 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
145 150 155 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
165 170 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
180 185 190

Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg
210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp
225 230 235 240

Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys
245 250 255

Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
260 265 270

Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
275 280 285

Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
290 295 300

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
305 310 315 320

Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly
325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln

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Glu Val Gln Pro Pro Val Thr Xaa Leu Ser Val
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<213> unknown

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<223> peptide motif found in many members of the haemopoietin receptor family

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